

Figure 9 shows a comparison between the amino acid sequences of PSEC67 (residues 61-730 of SEQ ID NO: 2) of the present invention and mouse FATP-3 (SEQ ID NO: 14).

Please delete the paragraph on page 17, lines 14-18, and replace it with the following paragraph:

Figure 10 shows the alignment of the amino acid sequences of PSEC67 (residues 61-730 of SEQ ID NO: 2) of the present invention (top) and human acyl-CoA synthetase (SEQ ID NO: 15)(bottom). The sequences underlined, YIFTSGTTGLPK (residues 332-343 of SEQ ID NO: 2) and FHDRTGDTFRWKGENVATTEVA (residues 587-608 of SEQ ID NO: 2), indicate ATP-binding region and conserved FATP region, respectively.

#### REMARKS

Applicants believe that the present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

Respectfully submitted,

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Date

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**MARKED UP VERSION OF AMENDED PARAGRAPHS**

**Marked up version of paragraph on page 17, lines 6-7, is below:**

Figure 6 shows a comparison between the nucleotide sequences of PSEC67 (residues 501-2251 of SEQ ID NO: 1) of the present invention and the cDNA encoding mouse FATP-3 (SEQ ID NO: 13).

**Marked up version of paragraph on page 17, lines 12-13, is below:**

Figure 9 shows a comparison between the amino acid sequences of PSEC67 (residues 61-730 of SEQ ID NO: 2) of the present invention and mouse FATP-3 (SEQ ID NO: 14).

**Marked up version of paragraph on page 17, lines 14-18, is below:**

Figure 10 shows the alignment of the amino acid sequences of PSEC67 (residues 61-730 of SEQ ID NO: 2) of the present invention (top) and human acyl-CoA synthetase (SEQ ID NO: 15) (bottom). The sequences underlined, YIFTSGTTGLPK (residues 332-343 of SEQ ID NO: 2) and FHDRTGDTFRWKGENVATTEVA (residues 587-608 of SEQ ID NO: 2), indicate ATP-binding region and conserved FATP region, respectively.